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<110> ZHOU, PENGBO  
HOWLEY, PETER M.

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<140> 09/415,795

<141> 1999-10-08

<150> 60/103,787

<151> 1998-10-09

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<170> PatentIn Ver. 2.1

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<212> PRT

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Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
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Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
      35             40             45

Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
      50             55             60

Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
      65             70             75             80

Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
      85             90             95

Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
      100            105            110

Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
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His	Gly	His	Ile	Asn	Ser	Tyr	Leu	Lys	Pro	Met	Leu	Gln	Arg	Asp	Phe
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Leu	Ser	Tyr	Leu	Asp	Ala	Lys	Ser	Leu	Cys	Ala	Ala	Glu	Leu	Val	Cys
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Gly	Glu	Met	Leu	Asn	Thr	Leu	Ile	His	His	Cys	Glu	Ala	Val	Leu	His
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 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp  
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&lt;211&gt; 4470

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

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&lt;210&gt; 6

&lt;211&gt; 1151

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 6

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<212> DNA

<213> *Saccharomyces cerevisiae*

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 ccattaatgg ttttgccgtc taattcaggc tacattagta gctttgtgtc agatgaacac 1920

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aaaattatta gtggtaatga tggttctgta aagttatggg atggttaggac tggaaagctg 1980
ttacgttttc tattaacaga cctcacaaaa atatggcatg tcgattttga tgctatgcgt 2040
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tcaagaccgt ag 2112

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<210> 10

<211> 703

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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Met Ser Leu Ser Arg Cys Pro Thr Asp Asn Ser Ser Ser Arg Ile Asn
 1          5          10          15

Ser Ser Val Pro Leu Ile Asn Ser Ser Ser Pro Ala Thr Pro Pro Glu
          20          25          30

Ser Phe Asp Pro Gln Val Phe Pro Ser Ser Leu Ile His Gly Asp Asn
          35          40          45

Leu Leu Pro Gln Asp Asp Gln Ile Ala Ser Asp Pro Arg Ser Glu Ser
 50          55          60

Asn Ser Cys Asn Gly Asn Thr Ser Ser Ser Leu Pro Cys Thr Asp Ser
 65          70          75          80

Tyr Gln Tyr Pro Leu Lys His Ser Cys Thr Pro Ser Phe Leu Arg Lys
          85          90          95

Phe Asn Glu Ser Ile Glu Asn Val Ser Tyr Lys Cys Leu Asp His Ser
          100          105          110

Pro Pro Asp Ser Val Pro Gly Asp Phe Ser Ile Ser Leu Val Pro Gln
          115          120          125

Arg Asn Phe Leu Tyr Ser His Ser Ser Leu Pro Pro Lys Ile Ile Ser
          130          135          140

Ile Asp Arg Asn Asn Arg Ile Lys Leu Asp Asn Ser Ile Ser Ser Asn
          145          150          155          160

Ser Asp Asn Phe Pro Pro Ser Pro Lys Val Asp Thr Ser Asn Thr Val
          165          170          175

Ser Pro Gly Ser Lys Pro Ile Ser Glu Asp Leu Glu Asp Leu Asn Leu
          180          185          190

Gln Ser Ile Val Gln Thr Phe Glu Asp Leu Pro Glu Gly Ile Gln Ser
          195          200          205

Tyr Ala Phe Phe Gln Leu Leu Arg Ser Cys Asn Arg Gln Ser Met Arg
          210          215          220

Leu Leu Leu Asn Glu Cys Glu Pro Leu Leu Lys Lys Asp Ile Leu Ser
          225          230          235          240

Asn Leu Pro Phe Ser Ile Val Gln Ser Ile Leu Leu Asn Leu Asp Ile
          245          250          255

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His	Ser	Phe	Leu	Ser	Cys	Arg	Leu	Val	Ser	Pro	Thr	Trp	Asn	Arg	Ile	260	265	270
Leu	Asp	Val	His	Thr	Ser	Tyr	Trp	Lys	His	Met	Phe	Ser	Leu	Phe	Gly	275	280	285
Phe	Gln	Ile	Asn	Glu	Asn	Asp	Trp	Lys	Tyr	Ala	Asn	Pro	Asn	Leu	Asn	290	295	300
Arg	Pro	Pro	Phe	Leu	His	Asn	Asp	Gln	Ile	Ser	Asp	Asp	Tyr	Phe	Pro	305	310	315
Glu	Ile	Phe	Lys	Arg	His	Phe	Leu	Asn	Arg	Lys	Arg	Trp	Leu	Phe	Pro	325	330	335
Ser	Ile	Pro	Pro	Ser	His	Leu	Ser	Phe	Pro	Ile	His	Val	Pro	Asn	Phe	340	345	350
Met	Ile	Thr	Ser	Leu	Leu	Leu	His	Lys	Asp	Arg	Ile	Ile	Thr	Thr	Ser	355	360	365
Gly	Ser	Gly	Thr	Ile	Gln	Ile	His	Asn	Ala	Ile	Thr	Gly	Val	Leu	Glu	370	375	380
Ala	Arg	Leu	Glu	Gly	His	Lys	Glu	Gly	Val	Trp	Ala	Val	Lys	Ile	His	385	390	395
Glu	Asn	Thr	Leu	Val	Ser	Gly	Ser	Ile	Asp	Lys	Thr	Val	Arg	Val	Trp	405	410	415
Asn	Ile	Glu	Lys	Ala	Lys	Cys	Thr	His	Ile	Phe	Arg	Gly	His	Ile	Ser	420	425	430
Ile	Ile	Arg	Cys	Leu	Glu	Ile	Leu	Val	Pro	Ser	Arg	Leu	Ile	Arg	His	435	440	445
Gly	Val	Glu	Ile	Val	Glu	Pro	Asp	Gln	Pro	Tyr	Ile	Val	Ser	Gly	Ser	450	455	460
Arg	Asp	His	Thr	Leu	Arg	Val	Trp	Lys	Leu	Pro	Lys	Asn	Thr	Asp	Pro	465	470	475
Pro	Tyr	Leu	Pro	Asp	Asn	Thr	Asn	Ser	Ile	Asp	Arg	Trp	Glu	Lys	Asn	485	490	495
Pro	Tyr	Phe	Val	His	Thr	Leu	Ile	Gly	His	Thr	Asp	Ser	Val	Arg	Thr	500	505	510
Ile	Ser	Gly	Tyr	Gly	Asp	Ile	Leu	Val	Ser	Gly	Ser	Tyr	Asp	Ser	Ser	515	520	525
Ile	Arg	Ile	Trp	Arg	Val	Ser	Thr	Gly	Glu	Cys	Leu	Tyr	His	Leu	Arg	530	535	540
Gly	His	Ser	Leu	Arg	Ile	Tyr	Ser	Val	Leu	Tyr	Glu	Pro	Glu	Arg	Asn	545	550	555
Ile	Cys	Ile	Ser	Gly	Ser	Met	Asp	Lys	Ser	Ile	Arg	Val	Trp	Asp	Leu	565	570	575

Ser Thr Gly Thr Cys Lys Tyr Val Leu Glu Gly His Asp Ala Phe Val  
580 585 590

Thr Leu Leu Asn Val Phe Gln Asn Arg Leu Ile Ser Gly Ser Ala Asp  
595 600 605

Ser Thr Ile Arg Ile Trp Asp Leu Asn Thr Gly Lys Pro Leu Met Val  
610 615 620

Leu Pro Ser Asn Ser Gly Tyr Ile Ser Ser Phe Val Ser Asp Glu His  
625 630 635 640

Lys Ile Ile Ser Gly Asn Asp Gly Ser Val Lys Leu Trp Asp Val Arg  
645 650 655

Thr Gly Lys Leu Leu Arg Phe Leu Leu Thr Asp Leu Thr Lys Ile Trp  
660 665 670

His Val Asp Phe Asp Ala Met Arg Cys Val Ala Ala Val Gln Arg Asp  
675 680 685

Asp Gln Ala Tyr Leu Glu Val Ile Asn Phe Ser Gly Ser Arg Pro  
690 695 700

<210> 11  
<211> 2175  
<212> DNA  
<213> Mus sp.

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gccaaagcca aacttgccaa tggcacttcc agcatgattg tgcccaagca gcggaaactc 360  
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gagttggtac gctgcattcg atttgataac aaaaggatag tgagcggagc ctatgatggg 1560  
aaaattaaag tgtgggatct tatggctgct ttggaccggc gtgctccagc agggactctc 1620



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<210> 12  
 <211> 569  
 <212> PRT  
 <213> Mus sp.

<400> 12  
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 20 25 30  
 Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala  
 35 40 45  
 Arg Leu Cys Ile Asn Gln Glu Thr Val Cys Leu Thr Ser Thr Ala Met  
 50 55 60  
 Lys Thr Glu Asn Cys Val Ala Lys Ala Lys Leu Ala Asn Gly Thr Ser  
 65 70 75 80  
 Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys  
 85 90 95  
 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp  
 100 105 110  
 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln  
 115 120 125  
 His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe  
 130 135 140  
 Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile  
 145 150 155 160  
 Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys  
 165 170 175  
 Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu  
 180 185 190  
 Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu  
 195 200 205  
 Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Glu  
 210 215 220

Asn	Ala	Pro	Pro	Asn	Ser	Phe	Tyr	Arg	Ala	Leu	Tyr	Pro	Lys	Ile	Ile	225	230	235	240
Gln	Asp	Ile	Glu	Thr	Ile	Glu	Ser	Asn	Trp	Arg	Cys	Gly	Arg	His	Ser	245	250	255	
Leu	Gln	Arg	Ile	His	Cys	Arg	Ser	Glu	Thr	Ser	Lys	Gly	Val	Tyr	Cys	260	265	270	
Leu	Gln	Tyr	Asp	Asp	Gln	Lys	Ile	Val	Ser	Gly	Leu	Arg	Asp	Asn	Thr	275	280	285	
Ile	Lys	Ile	Trp	Asp	Lys	Ser	Thr	Leu	Glu	Cys	Lys	Arg	Ile	Leu	Thr	290	295	300	
Gly	His	Thr	Gly	Ser	Val	Leu	Cys	Leu	Gln	Tyr	Asp	Glu	Arg	Val	Ile	305	310	315	320
Ile	Thr	Gly	Ser	Ser	Asp	Ser	Thr	Val	Arg	Val	Trp	Asp	Val	Asn	Ala	325	330	335	
Gly	Glu	Met	Leu	Asn	Thr	Leu	Ile	His	His	Cys	Glu	Ala	Val	Leu	His	340	345	350	
Leu	Arg	Phe	Asn	Asn	Gly	Met	Met	Val	Thr	Cys	Ser	Lys	Asp	Arg	Ser	355	360	365	
Ile	Ala	Val	Trp	Asp	Met	Ala	Ser	Pro	Thr	Asp	Ile	Thr	Leu	Arg	Arg	370	375	380	
Val	Leu	Val	Gly	His	Arg	Ala	Ala	Val	Asn	Val	Val	Asp	Phe	Asp	Asp	385	390	395	400
Lys	Tyr	Ile	Val	Ser	Ala	Ser	Gly	Asp	Arg	Thr	Ile	Lys	Val	Trp	Asn	405	410	415	
Thr	Ser	Thr	Cys	Glu	Phe	Val	Arg	Thr	Leu	Asn	Gly	His	Lys	Arg	Gly	420	425	430	
Ile	Ala	Cys	Leu	Gln	Tyr	Arg	Asp	Arg	Leu	Val	Val	Ser	Gly	Ser	Ser	435	440	445	
Asp	Asn	Thr	Ile	Arg	Leu	Trp	Asp	Ile	Glu	Cys	Gly	Ala	Cys	Leu	Arg	450	455	460	
Val	Leu	Glu	Gly	His	Glu	Glu	Leu	Val	Arg	Cys	Ile	Arg	Phe	Asp	Asn	465	470	475	480
Lys	Arg	Ile	Val	Ser	Gly	Ala	Tyr	Asp	Gly	Lys	Ile	Lys	Val	Trp	Asp	485	490	495	
Leu	Met	Ala	Ala	Leu	Asp	Pro	Arg	Ala	Pro	Ala	Gly	Thr	Leu	Cys	Leu	500	505	510	
Arg	Thr	Leu	Val	Glu	His	Ser	Gly	Arg	Val	Phe	Arg	Leu	Gln	Phe	Asp	515	520	525	
Glu	Phe	Gln	Ile	Val	Ser	Ser	Ser	His	Asp	Asp	Thr	Ile	Leu	Ile	Trp	530	535	540	

Asp Phe Leu Asn Asp Pro Ala Ala His Ala Glu Pro Pro Arg Ser Pro  
 545 550 555 560

Ser Arg Thr Tyr Thr Tyr Ile Ser Arg  
 565

<210> 13  
 <211> 9  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: SV40 Large T antigen fragment

<400> 13  
 Pro Pro Lys Lys Lys Arg Lys Val Ala  
 1 5

<210> 14  
 <211> 32  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: formula  
 sequence

<220>  
 <221> MOD\_RES  
 <222> (3)...(6)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (7)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (8)...(9)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (10)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (11)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (12)  
 <223> aromatic amino acid

<220>  
 <221> MOD\_RES  
 <222> (13)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (14)...(16)  
 <223> amino acid which stabilizes a tight polypeptide backbone turn such as Gly, Pro, Asp or Asn

<220>  
 <221> MOD\_RES  
 <222> (17)  
 <223> polar amino acid

<220>  
 <221> MOD\_RES  
 <222> (18)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (19)...(20)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (21)...(24)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (26)...(29)  
 <223> any amino acid

<220>  
 <221> MOD\_RES  
 <222> (30)  
 <223> hydrophobic

<220>  
 <223> this sequence may also encompass a deletion peptide wherein certain positions are absent according to the disclosure

<400> 14  
 Gly His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
       1                  5                  10                  15  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Trp Asp  
                   20                  25                  30

<210> 15  
 <211> 12  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: EGF-derived

## peptide

&lt;400&gt; 15

Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys  
 1 5 10

&lt;210&gt; 16

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

<223> Description of Unknown Organism: EGF-derived  
 peptide

&lt;400&gt; 16

Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys  
 1 5 10

&lt;210&gt; 17

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: formula  
 sequence

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (1)

&lt;223&gt; unique amino acid, such as cys or lys

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (2)...(3)

<223> amino acid residue selected to modulate the affinity of  
 the internalizing peptide for different membranes

&lt;400&gt; 17

Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala  
 1 5 10 15

Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala  
 20 25 30

&lt;210&gt; 18

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

<223> Description of Unknown Organism: peptide substrate  
 for N-myristoyl transferase

<400> 18

Gly Asn Ala Ala Ala Ala Arg Arg  
1 5

<210> 19

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: peptide derived  
from laminin

<400> 19

Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys  
1 5 10

<210> 20

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NdeI-EcoRI fragment

<400> 20

catatgggtg gctgccgtgg cgatatgttc ggttgcggtg ctcctccaaa aaagaagaga 60  
aaggtagctg gattc 75

<210> 21

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: RGD/SV40 peptide

<400> 21

Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys  
1 5 10 15

Lys Lys Arg Lys Val Ala Gly Phe  
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<210> 22

<211> 225

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NdeI-EcoRI fragment

<400> 22

catatgggagc cagtagatcc tagactagag ccctggaagc atccaggaag tcagcctaaa 60  
actgcttgta ccaattgcta ttgtaaaaag tgttgctttc attgccaagt ttgtttcata 120

acaaaagccc ttggcatctc ctatggcagg aagaagcgga gacagcgacg aagacctctt 180  
 caaggcagtc agactcatca agtttctcta agtaagcaag gattc 225

<210> 23  
 <211> 72  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: engineered HIV-1 tat

<400> 23  
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
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 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
                   20                  25                  30  
 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly  
           35                  40                  45  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
           50                  55                  60  
 His Gln Val Ser Leu Ser Lys Gln  
           65                  70

<210> 24  
 <211> 912  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: NdeI-EcoRI fragment

<400> 24  
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 tcccgccgtg gcgccctaca gacacgctcg cgccagaggg gcgaggtccg ttctgtccag 180  
 tacgacgagt cggattatgc cctctacggg ggctcgtcat ccgaagacga cgaacacccg 240  
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 cgggcgcctc cgccacccgc tgggtccgga ggggcgggac gcacacccac caccgcccc 360  
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 aatccagacg tgggtgcagga cgtcgacgcg gccacggcga ctcgagggcg ttctgcggcg 840  
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 gtcgaggaat tc 912

<210> 25  
 <211> 301  
 <212> PRT  
 <213> Artificial Sequence

<223> Description of Artificial Sequence: engineered HSV-1 VP22

Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro Arg  
1 5 10 15

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg  
35 40 45

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu  
65 70 75 80

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly  
100 105 110

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys  
130 135 140

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu  
165 170 175

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu  
195 200 205

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr  
225 230 235 240

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala  
260 265 270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala  
275 280 285



Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu  
 290 295 300

<210> 26  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 26  
 catatggacg tcgacgcggc cacggcgact cgagggcggt ctgcggcgct gcgccccacc 60  
 gagcgacctc gagccccagc ccgctccgct tctcgcccca gacggcccgt cgaggaattc 120

<210> 27  
 <211> 37  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: VP22 (C-terminal domain)

<400> 27  
 Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser  
 1 5 10 15  
 Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro  
 20 25 30  
 Arg Arg Pro Val Glu  
 35

<210> 28  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Linker peptide

<400> 28  
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
 1 5 10 15

<210> 29  
 <211> 4  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: tetrapeptide isostere

<400> 29  
 Ala Ile Tyr Tyr  
 1

<210> 30  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 30  
 gcggatccac catggataam aaagagggac ctaataac 38

<210> 31  
 <211> 76  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 31  
 gcgcggccgc ctactcatca tcactagatg gcamcttctg agcaaaacag ccctctggta 60  
 ttatagttgt cctcgt 76

<210> 32  
 <211> 72  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 32  
 cgcgccgcc tactcatcat cactagatgg camttgagcc aaagttttct ctggtattat 60  
 agttgtcctc gt 72

<210> 33  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> modified\_base  
 <222> (20)  
 <223> i

<220>  
 <223> Description of Artificial Sequence: primer

<400> 33  
 gcwatccacc atggataatn taaagagga cctaataac 39

<210> 34  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 34  
 gtagtgtat ctccatgtgg tatratagtr gtcc

34

<210> 35  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 35  
 ggacaactat aataccacat ggagatacac ctac

34

<210> 36  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 36  
 gcctcgagtc actcctcctc tgagctgtc

29

<210> 37  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 37  
 gcggatccac catggataam aaagaggac ctaataac

38

<210> 38  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 38  
 cctatcacat ctatatttta ttggtattat agttgtc

37

<210> 39  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 39  
 gacaactata ataccaataa aatatagatg tgatagg 37

<210> 40  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 40  
 gcctcgagtc ataatgtgtt agtatattgt cctg 34

<210> 41  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 41  
 gcggatccac catggaggaa gaagagtata tgcccatgga ggagactctt tgccaacggt 60  
 ttaaatgtg 69

<210> 42  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 42  
 gcgcggccgc tcatatagac ataaatccag tagac 35

<210> 43  
 <211> 65  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 43  
 gcggatccgc caccatggac tacaaggacg acgatgacaa agatgacccg gccgaggcgg 60

tgctg

65

&lt;210&gt; 44

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 44

gtaggtgtat ctccatgtct ggagatgtag gtgtatg

37

&lt;210&gt; 45

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 45

catacaccta catctccaga catggagata cacctac

37

&lt;210&gt; 46

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 46

gcgcggccgc tcactcctcc tctgagctgt c

31

&lt;210&gt; 47

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: LFCSE motif

&lt;400&gt; 47

Leu Phe Cys Ser Glu

1

5

&lt;210&gt; 48

&lt;211&gt; 2151

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (70)..(1779)

<400> 48  
 tgcgttggct gcggcctggc accaaagggg cgccccggc ggagagcgga cccagtggcc 60  
 tcggcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 111  
           Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys  
           1                  5                  10  
 ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct 159  
 Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro  
 15                  20                  25                  30  
 agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc 207  
 Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser  
                   35                  40                  45  
 tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act 255  
 Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr  
                   50                  55                  60  
 gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc 303  
 Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly  
                   65                  70                  75  
 act tcc agt atg att gtg ccc aag caa cgg aaa ctc tca gca agc tat 351  
 Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr  
                   80                  85                  90  
 gaa aag gaa aag gaa ctg tgt gtc aaa tac ttt gag cag tgg tca gag 399  
 Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu  
                   95                  100                  105                  110  
 tca gat caa gtg gaa ttt gtg gaa cat ctt ata tcc caa atg tgt cat 447  
 Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His  
                   115                  120                  125  
 tac caa cat ggg cac ata aac tcg tat ctt aaa cct atg ttg cag aga 495  
 Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg  
                   130                  135                  140  
 gat ttc ata act gct ctg cca gct cgg gga ttg gat cat atc gct gag 543  
 Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu  
                   145                  150                  155  
 aac att ctg tca tac ctg gat gcc aaa tca cta tgt gct gct gaa ctt 591  
 Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu  
                   160                  165                  170  
 gtg tgc aag gaa tgg tac cga gtg acc tct gat ggc atg ctg tgg aag 639  
 Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys  
                   175                  180                  185                  190  
 aag ctt atc gag aga atg gtc agg aca gat tct ctg tgg aga ggc ctg 687  
 Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu  
                   195                  200                  205  
 gca gaa cga aga gga tgg gga cag tat tta ttc aaa aac aaa cct cct 735  
 Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro  
                   210                  215                  220

gac ggg aat gct cct ccc aac tct ttt tat aga gca ctt tat cct aaa	783
Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys	
225 230 235	
att ata caa gac att gag aca ata gaa tct aat tgg aga tgt gga aga	831
Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg	
240 245 250	
cat agt tta cag aga att cac tgc cga agt gaa aca agc aaa gga gtt	879
His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val	
255 260 265 270	
tac tgt tta cag tat gat gat cag aaa ata gta agc ggc ctt cga gac	927
Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp	
275 280 285	
aac aca atc aag atc tgg gat aaa aac aca ttg gaa tgc aag cga att	975
Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile	
290 295 300	
ctc aca ggc cat aca ggt tca gtc ctc tgt ctc cag tat gat gag aga	1023
Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg	
305 310 315	
gtg atc ata aca gga tca tgc gat tcc acg gtc aga gtg tgg gat gta	1071
Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val	
320 325 330	
aat aca ggt gaa atg cta aac acg ttg att cac cat tgt gaa gca gtt	1119
Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val	
335 340 345 350	
ctg cac ttg cgt ttc aat aat ggc atg atg gtg acc tgc tcc aaa gat	1167
Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp	
355 360 365	
cgt tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc	1215
Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu	
370 375 380	
cgg agg gtg ctg gtc gga cac cga gct gct gtc aat gtt gta gac ttt	1263
Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe	
385 390 395	
gat gac aag tac att gtt tct gca tct ggg gat aga act ata aag gta	1311
Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val	
400 405 410	
tgg aac aca agt act tgt gaa ttt gta agg acc tta aat gga cac aaa	1359
Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys	
415 420 425 430	
cga ggc att gcc tgt ttg cag tac agg gac agg ctg gta gtg agt ggc	1407
Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly	
435 440 445	
tca tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt	1455
Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys	
450 455 460	

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tta cga gtg tta gaa ggc cat gag gaa ttg gtg cgt tgt att cga ttt      1503
Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe
      465                      470                      475

gat aac aag agg ata gtc agt ggg gcc tat gat gga aaa att aaa gtg      1551
Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val
      480                      485                      490

tgg gat ctt gtg gct gct ttg gac ccc cgt gct cct gca ggg aca ctc      1599
Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu
      495                      500                      505                      510

tgt cta cgg acc ctt gtg gag cat tcc gga aga gtt ttt cga cta cag      1647
Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln
      515                      520                      525

ttt gat gaa ttc cag att gtc agt agt tca cat gat gac aca atc ctc      1695
Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu
      530                      535                      540

atc tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt      1743
Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg
      545                      550                      555

tcc cct tct cga aca tac acc tac atc tcc aga taa ataaccatac      1789
Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
      560                      565

actgacctca tacttgccca ggaccatta aagttgcggt atttaacgta tctgccata      1849

ccaggatgag caacaacagt aacaatcaaa ctactgccca gtttccctgg actagccgag      1909

gagcagggct ttgagactcc tggtgggaca cagttggtct gcagtcggcc caggacggtc      1969

tactcagcac aactgactgc ttcagtgtg ctatcagaag atgtcttcta tcaattgtga      2029

atgattggaa cttttaaac tcccctcctc tcctcctttc acctctgcac ctagtttttt      2089

cccattgggt ccagacaaag gtgacttata aatatattta gtgttttgcc agaaaaaaaa      2149

aa                                                                 2151

<210> 49
<211> 569
<212> PRT
<213> Homo sapiens

<400> 49
Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
1          5          10          15

Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
20          25          30

Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
35          40          45

```



Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met  
50 55 60

Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser  
65 70 75 80

Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys  
85 90 95

Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp  
100 105 110

Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln  
115 120 125

His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe  
130 135 140

Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile  
145 150 155 160

Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys  
165 170 175

Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu  
180 185 190

Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu  
195 200 205

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly  
210 215 220

Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile  
225 230 235 240

Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser  
245 250 255

Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys  
260 265 270

Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr  
275 280 285

Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr  
 290 295 300

Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile  
 305 310 315 320

Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr  
 325 330 335

Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His  
 340 345 350

Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser  
 355 360 365

Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg  
 370 375 380

Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp  
 385 390 395 400

Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn  
 405 410 415

Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly  
 420 425 430

Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser  
 435 440 445

Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg  
 450 455 460

Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn  
 465 470 475 480

Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp  
 485 490 495

Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu  
 500 505 510

Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp  
 515 520 525

Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp  
530 535 540

Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro  
545 550 555 560

Ser Arg Thr Tyr Thr Tyr Ile Ser Arg  
565